

EXHIBIT 9

ATGTC

-145 CATGAAGTGC TGAGTGGATA AACAGCACGG GATATCTCTG TCTAAAGGAA TATTACTACA CCAGGAAAAG

-140 GACACATTCC ACAACAGGAA AGGAGCCTGT CACAGAAAAC CACAGTCTCC TGTGCATGTG ACATTTCCGC

-70 ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG GGC TGT GAG AAG 60

1 Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Val Gly Cys Glu Lys 20

61 GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TGT CAG CCT GGT ACT TTC TGC AGA AAA TAC 120

21 Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys Tyr 40

121 AAT CCA GTC TGC AAG AGC TGC CCT CCA AGT AGC TTC TCC AGC ATA GGT GGA CAG CCG AAC 180

41 Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ile Gly Gly Gln Pro Asn 60

181 TGT AAC ATC TGC AGA CTC TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT AGC 240

61 Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr 80

241 CAC AAC GGC GAG TGT GAG TCC ATT GAA GGA TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA 300

81 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg 100

301 TGT GAA AAG GAC TGC AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC 360

101 Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser 120

361 TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC TGG AGG AAC TGC TCT 420

121 Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser 140

421 CTA GAC GGA AGG TCT GTC CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC 480

141 Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro 160

481 CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA 540

161 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly 180

541 GGG CAC TCC TTG CAG CTC CTT ACC TTG TTC CTG GCG CTA TCG GCT TTG CTG CTG GCC 600

181 Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser Ala Leu Leu Leu Ala 200

601 CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC 660

201 Leu Ile Phe Ile Thr Leu Leu Phe Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His 220

661 ATA TTC AAG CAA CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC 720

221 Ile Phe Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser 240

721 TGC CGA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGC TAT GAG CTG TGA TGTACTATC 780

241 Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu ---

781 CTAGGAGATG TGTGGGCGGA AACCGAGAAG CACTAGGACC CCACCATCCT GTGGAACAGC ACAAGCAACC 850

851 CCACCACCCT GTTCTTACAC ATCATCTAG ATGATGTGTG GCGCGGCACC TCATCCAAGT CTCTTCTAAC 920

921 GCTAACATAT TGTCTTTTAC CTTTTTTTAA TCTTTTTTTA AATTTAAATT TTATGTGTGT GAGTGTTTTG 990

991 CCTGCCGTGA TGCACACGTG TGTGTGTGTG TGTGTGTGAC ACTCCTGATG CCTGAGGAGG TCAGAAAGAGA 1060

1061 AAGGGTTGGT TCCATAAGAA CTGGAGTTAT GGATGGCTGT GAGCCGnnnn GATAGGTGCG CACGGAGACC 1130

1131 TGTCTTCTTA TTTTAACTGT ACTGTATAT AAAAATAAAA TGATATTTTC GGAATTTAG AGATTGCTCT 1200

1201 GACACCCTTC TAGTTAATGA TCTAAGAGGA ATTGTTGATA CGTAGTATAC TGTATATGTG TATGTATATG 1270

1271 TATATGTATA TATAAGACTC TTTTACTGTC AAAGTCAACC TAGAGTGTCT GGTACCAGG TCAATTTTAT 1340

1341 TGGACATTTT ACGTCACACA CACACACACA CACACACACA CACGTTTATA CTACGTACTGT TATCGGTAT 1410

1411 TCTACGTCAT ATAATGGGAT AGGGTAAAAG GAAACCAAAG AGTGAGTGAT ATTATTGTGGA GGTGACAGA 1480

1481 CTACCCCTTC TGGGTACGTA GGGACAGACC TCCTTCGGAC TGTCTAAAAC TCCCTTAGA AGTCTCGTCA 1550

1551 AGTTCCCGGA CGAAGAGGAC AGAGGAGACA CAGTCCGAAA AGTTATTTTT CCGGCAAAATC CTTTCCCTGT 1620

1621 TTCGTGACAC TCCACCCCTT GTGGACACTT GAGTGTCTAT CTTCGCGCGG AAGGTCAGGT GGTACCCGTC 1690

1691 TGTAGGGGCG GGGAGACAGA GCGCGGGGGG AGCTACGAGA ATCGACTCAC AGGGCGCCCC GGGCTTCGGA 1760

1761 AATGAACTT TTTTATCTC ACAAGTTTCG TCCGGGCTCG GCGGACCTAT GCGGTGATC CTATTACCT 1830

1831 TATCCTGGCG CCAAGATAAA ACAACCAAAA GCCTTGACTC CGGTACTAAT TCTCCCTGCC GGGCCCCGTA 1900

1901 AGCATAACCG GGGCATCTCC ACTTTAAGAA CTTGGCGCGG TCTGCCTCG TCTCGCTTC GTAAACGGTT 1970

1971 CTTACAAAAG TAATTAGTTC TTGCTTTTCA CTTCAAGCT TCTGCTAGTC TAAGGACGA TCAAGGCTGG 2040

2041 TATTTGCTAC GGCTGACCGG TACGCGCGCG CAATAAGGCT ACTGGCGCGG CCGTCAAGG CCGTTTGGTT 2110

2111 TCAGAAACCC AAGGCCCCCC TCATACCAAC GTTTCGACTT TGATTCTTGC CGGTACGTGG TGGTGGGTGC 2180

2181 CTTAGCTCTT TCTCGATAGT TAG AC

328
105

273

Length
mouse

378

-105

273

GATT